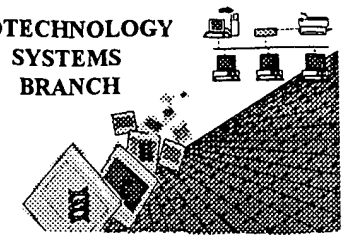
Connie wit

1627

BIOTECHNOLOGY
SYSTEMS
BRANCH



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RAW SEQUENCE LISTING ERROR REPORT

H22

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/653,761
Source: 1600 RUSH
Date Processed by STIC: 8/28/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/653,761

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

S. Ponnaluri

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1600

RAW SEQUENCE LISTING DATE: 08/28/2002
PATENT APPLICATION: **US/09/653,761** TIME: 09:52:27

Input Set : **A:\2719.2004-000 SUB SEQ.txt**
Output Set: **N:\CRF3\08282002\I653761.raw**

PP 1-6

Does Not Comply
Corrected Diskette Needed

```
 4 <110> APPLICANT: Fodor, Stephen P.A.
 5       Read, J. Leighton
 6       Stryer, Lubert
 7       Pirrung, Michael C.
 9 <120> TITLE OF INVENTION: Polypeptide Arrays (As Amended)
12 <130> FILE REFERENCE: 2719.2004-000
14 <140> CURRENT APPLICATION NUMBER: 09/653,761
15 <141> CURRENT FILING DATE: 2000-09-01
17 <150> PRIOR APPLICATION NUMBER: 09/557,875
18 <151> PRIOR FILING DATE: 2000-04-24
20 <150> PRIOR APPLICATION NUMBER: 09/056,927
21 <151> PRIOR FILING DATE: 1998-04-08
23 <150> PRIOR APPLICATION NUMBER: 08/670,118
24 <151> PRIOR FILING DATE: 1996-06-25
26 <150> PRIOR APPLICATION NUMBER: 08/168,904
27 <151> PRIOR FILING DATE: 1993-12-15
29 <150> PRIOR APPLICATION NUMBER: 07/624,114
30 <151> PRIOR FILING DATE: 1990-12-06
32 <150> PRIOR APPLICATION NUMBER: 07/362,901
33 <151> PRIOR FILING DATE: 1989-06-07
35 <150> PRIOR APPLICATION NUMBER: 07/492,462
36 <151> PRIOR FILING DATE: 1990-03-07
38 <150> PRIOR APPLICATION NUMBER: 08/348,471
39 <151> PRIOR FILING DATE: 1994-11-30
41 <150> PRIOR APPLICATION NUMBER: 07/805,727
42 <151> PRIOR FILING DATE: 1991-12-06
44 <150> PRIOR APPLICATION NUMBER: 07/624,120
45 <151> PRIOR FILING DATE: 1990-12-06
47 <160> NUMBER OF SEQ ID NOS: 34
49 <170> SOFTWARE: FastSEQ for Windows Version 4.0
51 <210> SEQ ID NO: 1
52 <211> LENGTH: 5
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Peptide
59 <400> SEQUENCE: 1
60 Tyr Gly Gly Phe Leu
61  1               5
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 4
66 <212> TYPE: PRT
67 <213> ORGANISM: Artificial Sequence
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(global error)
insufficient explanation - please give source of genetic material (see item 11 on Error Summary Sheet

RAW SEQUENCE LISTING
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DATE: 08/28/2002
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Input Set : A:\2719.2004-000 SUB SEQ.txt
Output Set: N:\CRF3\08282002\I653761.raw

same error

69 <220> FEATURE:
70 <223> OTHER INFORMATION: Peptide
72 <400> SEQUENCE: 2
73 Gly Gly Phe Leu
74 1
77 <210> SEQ ID NO: 3
78 <211> LENGTH: 5
79 <212> TYPE: PRT
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Peptide
85 <400> SEQUENCE: 3
86 Pro Gly Gly Phe Leu
87 1 5
90 <210> SEQ ID NO: 4
91 <211> LENGTH: 6
92 <212> TYPE: PRT
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Peptide
98 <400> SEQUENCE: 4
99 Tyr Pro Gly Gly Phe Leu
100 1 5
103 <210> SEQ ID NO: 5
104 <211> LENGTH: 5
105 <212> TYPE: PRT
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Peptide
111 <400> SEQUENCE: 5
112 Tyr Ala Gly Phe Leu
113 1 5
116 <210> SEQ ID NO: 6
117 <211> LENGTH: 5
118 <212> TYPE: PRT
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Peptide
124 <400> SEQUENCE: 6
125 Tyr Ser Gly Phe Leu
126 1 5
129 <210> SEQ ID NO: 7
130 <211> LENGTH: 5
131 <212> TYPE: PRT
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Peptide
137 <400> SEQUENCE: 7
138 Leu Gly Gly Phe Leu

RAW SEQUENCE LISTING
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Input Set : A:\2719.2004-000 SUB SEQ.txt
Output Set: N:\CRF3\08282002\I653761.raw

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139  1               5
142 <210> SEQ ID NO: 8
143 <211> LENGTH: 5
144 <212> TYPE: PRT
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Peptide
150 <400> SEQUENCE: 8
151 Phe Gly Gly Phe Leu
152  1               5
155 <210> SEQ ID NO: 9
156 <211> LENGTH: 5
157 <212> TYPE: PRT
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Peptide
163 <400> SEQUENCE: 9
164 Leu Ala Gly Phe Leu
165  1               5
168 <210> SEQ ID NO: 10
169 <211> LENGTH: 5
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Peptide
176 <400> SEQUENCE: 10
177 Phe Ala Gly Phe Leu
178  1               5
181 <210> SEQ ID NO: 11
182 <211> LENGTH: 5
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Peptide
189 <400> SEQUENCE: 11
190 Trp Gly Gly Phe Leu
191  1               5
194 <210> SEQ ID NO: 12
195 <211> LENGTH: 5
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Peptide
202 <400> SEQUENCE: 12
203 Tyr Pro Gly Phe Leu
204  1               5
207 <210> SEQ ID NO: 13
208 <211> LENGTH: 5
209 <212> TYPE: PRT
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Input Set : A:\2719.2004-000 SUB SEQ.txt
Output Set: N:\CRF3\08282002\I653761.raw

210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Peptide
215 <400> SEQUENCE: 13
216 Leu Pro Gly Phe Leu
217 1 5
220 <210> SEQ ID NO: 14
221 <211> LENGTH: 5
222 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Peptide
228 <400> SEQUENCE: 14
229 Trp Pro Gly Phe Leu
230 1 5
233 <210> SEQ ID NO: 15
234 <211> LENGTH: 5
235 <212> TYPE: PRT
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Peptide
241 <400> SEQUENCE: 15
242 Trp Ala Gly Phe Leu
243 1 5
246 <210> SEQ ID NO: 16
247 <211> LENGTH: 5
248 <212> TYPE: PRT
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Peptide
254 <400> SEQUENCE: 16
255 Leu Ser Gly Phe Leu
256 1 5
259 <210> SEQ ID NO: 17
260 <211> LENGTH: 5
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Peptide
267 <400> SEQUENCE: 17
268 Phe Ser Gly Phe Leu
269 1 5
272 <210> SEQ ID NO: 18
273 <211> LENGTH: 5
274 <212> TYPE: PRT
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Peptide
280 <400> SEQUENCE: 18

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/653,761

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Input Set : A:\2719.2004-000 SUB SEQ.txt
Output Set: N:\CRF3\08282002\I653761.raw

```
281 Trp Ser Gly Phe Leu
282  1               5
285 <210> SEQ ID NO: 19
286 <211> LENGTH: 5
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Peptide
293 <400> SEQUENCE: 19
294 Phe Pro Gly Phe Leu
295  1               5
298 <210> SEQ ID NO: 20
299 <211> LENGTH: 5
300 <212> TYPE: PRT
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Peptide containing D- amino acid
W--> 306 <221> NAME/KEY: VARIANT
307 <222> LOCATION: (2)...(2)
308 <223> OTHER INFORMATION: Xaa = D amino acid alanine
W--> 310 <400> 20
W--> 311 Tyr Xaa Gly Phe Leu
312  1               5
315 <210> SEQ ID NO: 21
316 <211> LENGTH: 5
317 <212> TYPE: PRT
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Peptide containing D- amino acid
W--> 323 <221> NAME/KEY: VARIANT
324 <222> LOCATION: (2)...(2)
325 <223> OTHER INFORMATION: Xaa = D amino acid serine
W--> 327 <400> 21
W--> 328 Tyr Xaa Gly Phe Leu
329  1               5
332 <210> SEQ ID NO: 22
333 <211> LENGTH: 5
334 <212> TYPE: PRT
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Peptide containing D- amino acid
W--> 340 <221> NAME/KEY: VARIANT
341 <222> LOCATION: (2)...(2)
342 <223> OTHER INFORMATION: Xaa = D amino acid proline
W--> 344 <400> 22
W--> 345 Tyr Xaa Gly Phe Leu
346  1               5
349 <210> SEQ ID NO: 23
350 <211> LENGTH: 5
```

does not explain source of genetic material

same error

same

Please correct any similar errors in subsequent sequences

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/28/2002
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Input Set : A:\2719.2004-000 SUB SEQ.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; Xaa Pos. 2
Seq#:21; Xaa Pos. 2
Seq#:22; Xaa Pos. 2
Seq#:23; Xaa Pos. 1
Seq#:24; Xaa Pos. 1
Seq#:25; Xaa Pos. 1,2
Seq#:26; Xaa Pos. 1
Seq#:27; Xaa Pos. 1,2
Seq#:28; Xaa Pos. 1,2
Seq#:29; Xaa Pos. 1,2
Seq#:30; Xaa Pos. 1,2
Seq#:31; Xaa Pos. 1,2
Seq#:32; Xaa Pos. 1,2
Seq#:33; Xaa Pos. 1,2
Seq#:34; Xaa Pos. 1,2

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/653,761

DATE: 08/28/2002
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Input Set : A:\2719.2004-000 SUB SEQ.txt
Output Set: N:\CRF3\08282002\I653761.raw

L:306 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:310 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:20
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:323 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:327 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:340 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:344 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:22
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:357 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:361 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:374 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:378 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:391 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:395 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:399 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:412 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:429 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:433 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
L:437 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:450 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:454 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:458 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:471 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:475 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:479 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:492 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:496 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:30
L:500 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:30
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:513 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:31
L:521 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:31
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:534 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:538 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:542 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:555 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:559 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33

VERIFICATION SUMMARY DATE: 08/28/2002
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Input Set : A:\2719.2004-000 SUB SEQ.txt
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L:563 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:576 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:580 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:584 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0

Application No.: 09/653,761

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

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